

103 86.5 3.5 489 2 B69964 probable glucose-6  
104 86.5 3.5 498 2 B99946 hypothetical prote  
105 86.5 3.5 912 1 RDBHNS nitrate reductase  
106 86.5 3.5 986 2 S77056 DNA-directed DNA p  
107 86 3.5 368 2 D90607 hypothetical prote  
108 86 3.5 370 2 G97277 glycosyltransferas  
109 86 3.5 470 2 B90481 glycosyltransferas  
110 86 3.5 498 2 AE1103 lysyl-tRNA synthet  
111 86 3.5 697 1 S04987 Sits-binding prote  
112 86 3.5 797 2 T50072 hypothetical prote  
113 86 3.5 831 2 T00323 chitinase (EC 3.2.  
114 86 3.5 875 2 T12794 hypothetical yomg  
115 86 3.5 880 2 S45627 regulatory protein  
116 86 3.5 1212 2 A84500 probable retroelem  
117 86 3.5 1513 2 A54768 mitotic spindle pr  
118 85.5 3.5 337 2 S74044 hypothetical prote  
119 85.5 3.5 455 2 G70089 hypothetical prote  
120 85.5 3.5 494 2 A47494 cytochrome P450 2A

## ALIGNMENTS

## \* RESULT 1

B49993  
glycylpeptide N-tetradecanoyltransferase (EC 2.3.1.97) - *Ajellomyces capsulata*  
C:Species: *Ajellomyces capsulata*, Histoplasma capsulatum  
C>Date: 10-Nov-1995 #sequence\_revision 10-Nov-1995 #text\_change 28-Jul-2000  
C:Accession: B49993  
R:Klodge, J.K.; Johnson, R.L.; Weinberg, R.A.; Gordon, J.I.  
J. Biol. Chem. 269, 2996-3009, 1994  
A:Title: Comparison of myristoyl-CoA:protein N-myristoyltransferases from three pathogen  
A:Reference number: A49993; MUID:94132075; PMID:8300631  
A:Accession: B49993  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-529 <LDD>  
A:Cross-References: GB:I25118; NID:9407694; PID:9407695  
C:Genetics:  
A:Gene: Nmt  
C:Genetics:  
A:Introns: 203/2; 464/3  
A:Superfamily: Yeast glycylpeptide N-tetradecanoyltransferase  
C:Keywords: acyltransferase; coenzyme A

Query Match 75.0%; Score 1839.5; DB 2; Length 529;

Best Local Similarity 72.4%; Pred. No. 7.6e-137;  
Matches 336; Conservative 67; Mismatches 60; Indels 1; Gaps 1;

DB 1 MASELLENNPALNRETAGMDKRAAEAMRKANIAELITGLSYGKNOKMDASYKFMOTOP 60  
DB 66 MASELLENNPALNRETAGMDKRAAEAMRKANIAELITGLSYGKNOKMDASYKFMOTOP 125  
QY 61 VPRPDETSTDT-GGPRTKIIDPEKVSKEPDALLBGFEMWATLIDTNETELQELMDLLIYHY 119  
DB 126 VIRPDRSESPDPGRIKIYELDQVSRPIPLVDGFEMWATLIDDEADVKEYEYLLAHY 185  
QY 120 EDDNAMPFRYSOSFTLHMLMSPGKKKWHGVAATKSKVLASIGCVPTETLNRNOK 179  
DB 186 EDGSAFMEFNYSPALFMAKAPGKRMHGVAVKSSKGLVASIGCVPAELAVRGSLSK 245  
QY 180 VYEINELCIHKILRSKRLPVLKELTRCYLNGIYQAIYTAGVLPVPSVSSCRVHPL 239  
DB 246 VTEINELCVHKILRSKRLPVLKELTRCYLNGIYQAIYTAGVLPVPSVSSCRVHPL 305  
QY 240 DWLKLYEGESPLPAGSTAROIITKNHLPSTTSPGLRPMPEKIDIDVHLLIYLSHFA 299  
DB 306 DWLKLYEGESPLPAGSTAROIITKNHLPSTTSPGLRPMPEKIDIDVHLLIYLSHFA 365  
QY 300 LNOAFTRREVDHMLVHKPEYVKEQVWVAIVVEDETHKIDDFESFNLESTYONPKDN 359  
DB 366 LQIFRSREVDHMLVHKPEYVKEQVWVAIVVEDETHKIDDFESFNLESTYONPKDN 425  
QY 360 VRAAIVLYYATETAFETNMALKERLIMLMDALLIAKKHFPVFNAFLHDPNPLEBOL 419

DB 426 VKAAIVLYYATETAFETNMALKERLIMLMDALLIAKKHFPVFNAFLHDPNPLEBOL 485  
QY 420 KFGAGDQQLHFIYNTKTPAPPGVGNENKLPDEKRGVGIYVL 463  
DB 486 KFGAGDQQLHFIYNTKTPAPPGVGNENKLPDEKRGVGIYVL 529

## RESULT 2

T40150  
probable glycylpeptide N-tetradecanoyltransferase (EC 2.3.1.97) - fission yeast (*Schizosaccharomyces pombe*)  
C:Species: *Schizosaccharomyces pombe*  
C>Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 18-Aug-2000  
C:Accession: T40150  
R:Wood, V.; Rajandream, M.A.; Barrell, B.G.; Devlin, K.; Churcher, C.M.  
submitted to the EMBL Data Library, March 1998  
A:Reference number: Z21842  
A:Accession: T40150  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-466 <WOO>  
A:Cross-References: EMBL:AL022103; PTDN:CAA17891.1; GSPDB:GN00067; SPDB:SPBC262.11  
A:Experimental source: strain 972h-; cosmid c262  
C:Genetics:  
A:Gene: SPDB:SPBC262.11  
A:Map position: 2  
A:Introns: 63/1; 104/3; 401/3  
A:Superfamily: Yeast glycylpeptide N-tetradecanoyltransferase  
C:Keywords: acyltransferase; coenzyme A

Query Match 51.1%; Score 1253; DB 2; Length 466;

Best Local Similarity 51.7%; Pred. No. 9.4e-91;  
Matches 245; Conservative 76; Mismatches 125; Indels 28; Gaps 6;

QY 7 ENNPALNRETAGMDKRAAEAMRKANIAELITGLSYGKNOKMDASYKFMOTOP 58  
DB 4 ENNKMTKN-----SQDSSFSBGGIRELDLRLRSILKEKRAAPRTYEDFFKWT 56  
QY 59 QVPRPDETSTDTGGPIITIDP-----EKVSKEPDALLBGFEMWATLIDTNETELQELMDLL 114  
DB 57 QVPRPDETSTDTGGPIITIDP-----IDPNDINQVPRPDEYRLKFEFEMWATLIDTNETELQELMDLL 112  
QY 115 TYHYVEDDNNAMPFRYSOSFTLHMLMSPGKKKWHGVAATKSKVLASIGCVPTETLN 174  
DB 113 TENVEDDNNAMPFRYSOSFTLHMLMSPGKKKWHGVAATKSKVLASIGCVPTETLN 172  
QY 175 NOKL-KYVENELCIHKILRSKRLPVLKELTRCYLNGIYQAIYTAGVLPVPSVSSCR 233  
DB 173 DKILKCAEYNEFCIHKILRSKRLPVLKELTRCYLNGIYQAIYTAGVLPVPSVSSCR 232  
QY 234 YHRRPLDWLKLYEGESPLPAGSTAROIITKNHLPSTTSPGLRPMPEKIDIDVHLLIY 293  
DB 233 YHRRPLDWLKLYEGESPLPAGSTAROIITKNHLPSTTSPGLRPMPEKIDIDVHLLIY 292  
QY 294 YLSRPAIINQAFTEEDHMLVHKPEYVKEQVWVAIVVEDETHKIDDFESFNLESTY 353  
DB 293 YLSRPAIINQAFTEEDHMLVHKPEYVKEQVWVAIVVEDETHKIDDFESFNLESTY 352  
QY 354 NPKXIDNVRRAIVLYYATETAFETNMALKERLIMLMDALLIAKKHFPVFNAFLH 409  
DB 353 NPKXIDNVRRAIVLYYATETAFETNMALKERLIMLMDALLIAKKHFPVFNAFLH 412  
QY 410 HDNPLFLEQLKFGAGDQQLHFIYNTKTPAPPGVGNENKLPDEKRGVGIYVL 463  
DB 413 LDNNFLKDKLFGAGDQQLHFIYNTKTPAPPGVGNENKLPDEKRGVGIYVL 466

## RESULT 3

A40163  
glycylpeptide N-tetradecanoyltransferase (EC 2.3.1.97) - yeast (*Saccharomyces cerevisiae*)  
C:Species: *Saccharomyces cerevisiae*  
C>Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 28-Jul-2000